



## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:**

Application Serial Number: 10/559,434  
Source: PCT/10  
Date Processed by STIC: 12/16/2005

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENT IN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/24/05



## Raw Sequence Listing Error Summary

**ERROR DETECTED****SUGGESTED CORRECTION**SERIAL NUMBER: 10/559,434**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1  Wrapped Nucleic  
  Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2  Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3  Misaligned Amino  
  Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4  Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5  Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6  PatentIn 2.0  
  "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7  Skipped Sequences  
  (OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8  Skipped Sequences  
  (NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9  Use of n's or Xaa's  
  (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10  Invalid <213>  
  Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11  Use of <220>  
  
Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12  PatentIn 2.0  
  "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13  Misuse of n/Xaa      "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWP

08159

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/559,434

DATE: 12/16/2005  
TIME: 15:38:57

Input Set : A:\SEQUENCE LISTING.txt  
Output Set: N:\CRF4\12162005\J559434.raw

3 <110> APPLICANT: Degussa AG  
5 <120> TITLE OF INVENTION: Screening process for hydantoin racemases  
7 <130> FILE REFERENCE: 030115 AM  
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/559,434  
C--> 10 <141> CURRENT FILING DATE: 2005-12-05  
12 <160> NUMBER OF SEQ ID NOS: 16  
14 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply  
Corrected Diskette Needed  
(Pg-1,2,3,4,5)

## ERRORED SEQUENCES

156 <210> SEQ ID NO: 4 → found 236  
157 <211> LENGTH: 237  
158 <212> TYPE: PRT  
159 <213> ORGANISM: Artificial sequence  
W--> 160  
160 <223> OTHER INFORMATION: Description of the artificial sequence  
OK 162 <400> SEQUENCE: 4  
163 Met Arg Ile Leu Val Ile Asn Pro Asn Ser Ser Ala Leu Thr Glu  
164 1 5 10 15  
165 Ser Val Ala Asp Ala Ala Gln Gln Val Val Ala Thr Gly Thr Ile Ile  
166 20 25 30  
167 Ser Ala Ile Asn Pro Ser Arg Gly Pro Ala Val Ile Glu Gly Ser Phe  
168 35 40 45  
169 Asp Glu Ala Leu Ala Thr Phe His Leu Ile Glu Glu Val Glu Arg Ala  
170 50 55 60  
171 Glu Arg Glu Asn Pro Pro Asp Ala Tyr Val Ile Ala Cys Phe Arg Asp  
172 65 70 75 80  
173 Pro Gly Leu Asp Ala Val Lys Glu Leu Thr Asp Arg Pro Val Val Gly  
174 85 90 95  
175 Val Ala Glu Ala Ala Ile His Met Ser Ser Phe Val Ala Ala Thr Phe  
176 100 105 110  
177 Ser Ile Val Ser Ile Leu Pro Arg Val Arg Lys His Leu His Glu Leu  
178 115 120 125  
179 Val Arg Gln Ala Gly Ala Thr Asn Arg Leu Ala Ser Ile Lys Leu Pro  
180 130 135 140  
181 145 150 155 160  
182 165 170 175  
183 Ser Ile Val Leu Gly Cys Ala Gly Met Val Gly Phe Ala Arg Gln Leu  
184 180 185 190  
185 Ser Asp Glu Leu Gly Val Pro Val Ile Asp Pro Val Glu Ala Ala Cys

1BG7

Mandatory field  
Identifier is missing.  
Pls Insert.

Invalid Response  
What is the  
Source of  
Material?  
Pls See Item  
# 11 on  
Error Summary  
Sheet.

<210> 1  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Description of the artificial sequence  
Consensus sequence

<400> 1  
Phe Xaa Asp Xaa Gly Leu  
1 5

Pls explain 'Xaa' location which residue they represents.  
See Error explanation on page-6

RYI

The following errors shown exist throughout the sequence listing. Please check subsequent sequences for similar errors.

Copy no of the appl

Phe X<sub>1</sub> Asp X<sub>2</sub> GL

~~X<sub>2</sub>=S~~ X<sub>1</sub> = S or D 10

X<sub>2</sub> = P or T

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/559,434

DATE: 12/16/2005  
TIME: 15:38:57

Input Set : A:\SEQUENCE LISTING.txt  
Output Set: N:\CRF4\12162005\J559434.raw

```

200      195      200      205
202 Arg Val Ala Glu Ser Leu Val Ala Leu Gly Tyr Gln Thr Ser Lys Ala
203      210      215      220
205 Asn Ser Tyr Gln Lys Pro Thr Glu Lys Gln Tyr Leu
E--> 206 225      230      235
283 <210> SEQ ID NO: 6
284 <211> LENGTH: 237 → found 236
285 <212> TYPE: PRT
286 <213> ORGANISM: Artificial sequence
W--> 287 < 223> OTHER INFORMATION: Description of the artificial sequence 3CH11
E--> 289 <400> SEQUENCE: 6
290 Met Arg Ile Leu Val Ile Asn Pro Asn Ser Ser Ser Ala Leu Thr Glu
291     1          5          10          15
293 Ser Val Ala Asp Ala Ala Gln Gln Val Val Ala Thr Gly Thr Ile Ile
294     20          25          30
296 Ser Ala Ile Asn Pro Ser Arg Gly Pro Ala Val Ile Glu Gly Ser Phe
297     35          40          45
299 Asp Glu Ala Leu Ala Thr His Leu Ile Glu Glu Val Glu Arg Ala
300     50          55          60
302 Glu Arg Glu Asn Pro Pro Asp Ala Tyr Val Ile Ala Cys Phe Glu Asp
303     65          70          75          80
305 Pro Gly Leu Asp Ala Val Lys Glu Leu Thr Asp Arg Pro Val Val Gly
306     85          90          95
308 Val Ala Glu Ala Ala Ile His Met Ser Ser Phe Val Ala Ala Thr Phe
309     100         105         110
311 Ser Ile Val Ser Ile Leu Pro Arg Val Arg Lys His Leu His Glu Leu
312     115         120         125
314 Val Arg Gln Ala Gly Ala Thr Asn Arg Leu Ala Ser Ile Lys Leu Pro
315     130         135         140
317 Asn Leu Gly Val Met Ala Phe His Glu Asp Glu His Ala Ala Leu Glu
318 145         150         155         160
320 Thr Leu Lys Gln Ala Ala Lys Glu Ala Val Gln Glu Asp Gly Ala Glu
321     165         170         175
323 Ser Ile Val Leu Gly Cys Ala Gly Met Val Gly Phe Ala Arg Gln Leu
324     180         185         190
326 Ser Asp Glu Leu Gly Val Pro Val Ile Asp Pro Val Glu Ala Ala Cys
327     195         200         205
329 Arg Val Ala Glu Ser Leu Val Ala Leu Gly Tyr Gln Thr Ser Lys Ala
330     210         215         220
332 Asn Ser Tyr Gln Lys Pro Thr Glu Lys Gln Tyr Leu
E--> 333 225      230      235

```

412 <210> SEQ ID NO: 8

413 <211> LENGTH: 237

414 <212> TYPE: PRT

415 <213> ORGANISM: Artificial sequence

W--> 416 < 223> OTHER INFORMATION: Description of the artificial sequence: AE3

E--> 418 <400> SEQUENCE: 8

Insert 220?

3CH11

Some Error

p/s Insert 220?

AE3

Some Error